## FIGURE 1: ISS-pST gene construct

	. 1	GCTAGCATGG	CCCTGTGGAT	GCGCCTCCTG	CCCCTGCTGG	CGCTGCTGGC
5	51	CCTCTGGGGA	CCTGACCCAG	CCGCAGCCCT	CGAGATGTTT	CCAGCTATGC
	101	CACTTTCTTC	TCTGTTCGCT	AACGCTGTTC	TTCGGGCCCA	GCACCTGCAC
	151	CAACTGGCTG	CCGACACCTA	CAAGGAGTTT	GAGCGCGCCT	ACATCCCGGA
	201	GGGACAGAGG	TACTCCATCC	AGAACGCCCA	GGCTGCCTTC	TGCTTCTCGG
	251	AGACCATCCC	GGCCCCCACG	GGCAAGGACG	AGGCCCAGCA	GAGATCGGAC
10	301	GTGGAGCTGC	TGCGCTTCTC	GCTGCTGCTC	ATCCAGTCGT	GGCTCGGGCC
	351	CGTGCAGTTC	CTCAGCAGGG	TCTTCACCAA	CAGCCTGGTG	TTTGGCACCT
	401	CAGACCGCGT	CTACGAGAAG	CTGAAGGACC.	TGGAGGAGGG	CATCCAGGCC
	451	CTGATGCGGG	AGCTGGAGGA	TGGCAGCCCC	CGGGCAGGAC	AGATCCTCAA
	501	GCAAACCTAC	GACAAATTTG	ACACAAACTT	GCGCAGTGAT	GACGCGCTGC
15.	551	TTAAGAACTA	CGGGCTGCTC	TCCTGCTTCA	AGAAGGACCT	GCACAAGGCT
	601	GAGACATACC	TGCGGGTCAT	GAAGTGTCGC	CGCTTCGTGG	AGAGCAGCTG
	651	TGCCTTCTAG	TCTAGA (SE	Q ID NO:4)		

20 <u>ATG...GCC</u>- insulin secretory signal.

GCTAGC- Nhe I restriction site incorporated into construct in order to ligate into plasmid.

CTCGAG- Xho I restriction site incorporated into construct in order to ligate secretory signal and pST.

TCTAGA- Xba I restriction site incorporated into construct in order to ligate into plasmid.



#### FIGURE 2: ISS-pST peptide sequence.

- 1 MALWMRLLPL LALLALWGPD PAAALEMFPA MPLSSLFANA VLRAQHLHQL
- 51 AADTYKEFER AYIPEGQRYS IQNAQAAFCF SETIPAPTGK DEAQQRSDVE
- 101 LLRFSLLLIQ SWLGPVQFLS RVFTNSLVFG TSDRVYEKLK DLEEGIQALM
- 151 RELEDGSPRA GQILKQTYDK FDTNLRSDDA LLKNYGLLSC FKKDLHKAET
- 201 YLRVMKCRRF VESSCAF (SEQ ID NO:3)

10

MAL...AAA- insulin secretory signal, cleaved upon secretion of pST.

LE- function of XhoI cleavage site; result in no predicted secondary structural changes to pST.

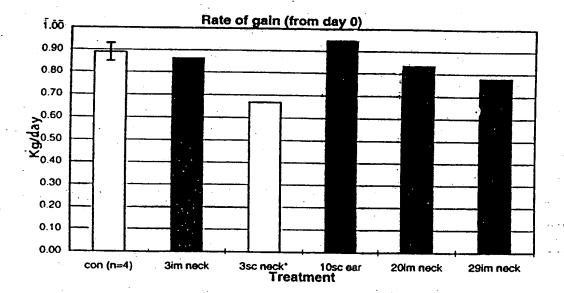


Figure 3

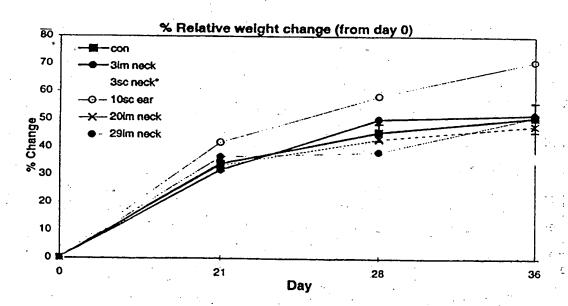
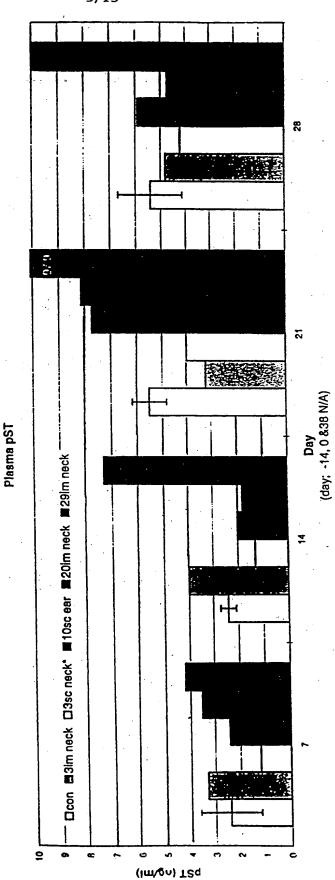


Figure 4

Figure 5



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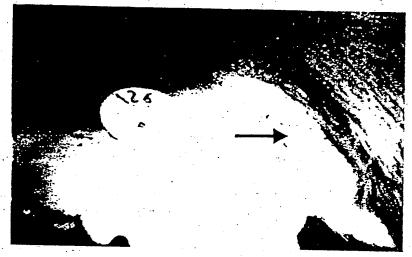
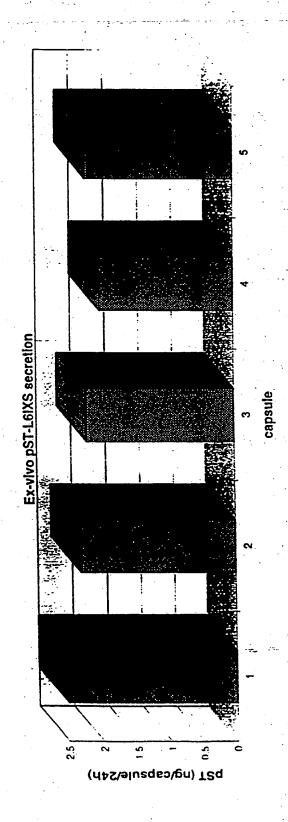


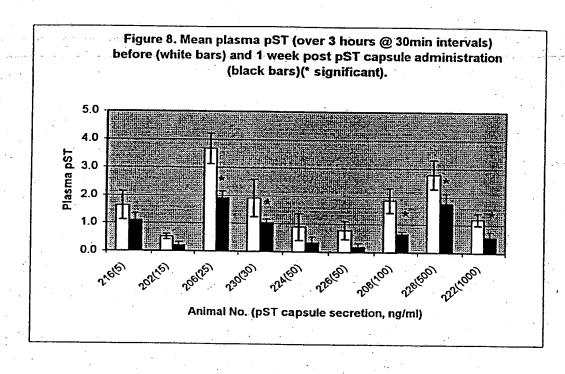
Plate 2

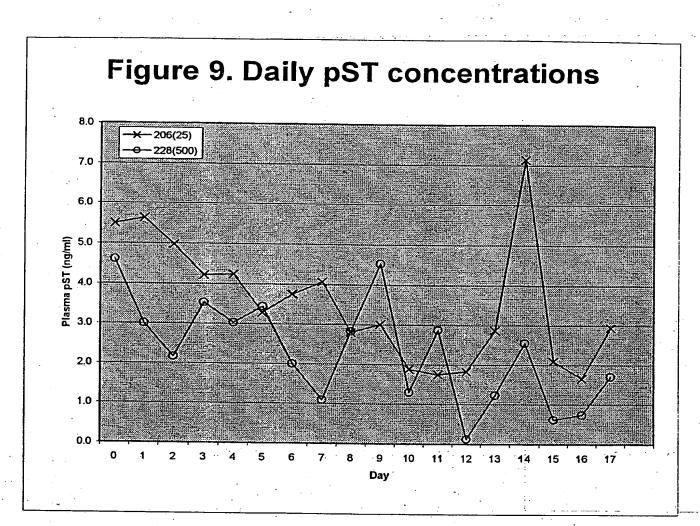


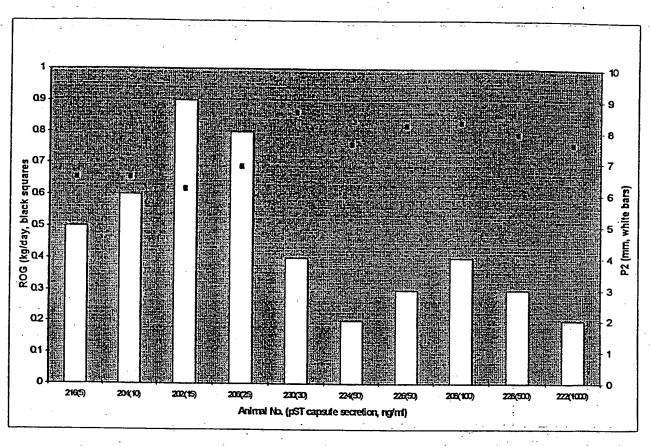
Figure 6

Figure 7









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